IN THE CLAIMS:

Please AMEND claims 1-7 as follows.

Please ADD claims 12-14 as follows.

1. (Currently Amended) A method, comprising:

introducing a genotype H^XH^X·Pg/pg·Cy/cy·Dp/dp in a flavonoid biosynthesis for crossing flowering plants to create a new flower color,

wherein the genotype H^XH^X·Pg/pg·Cy/cy·Dp/dp is an inheritance of flower pigments, pelargonidin (Pgn), cyanidin (Cyn), and delphinidin (Dpn), for a flower color expression, and

wherein five multiple alleles, H^T, H^F, H^D, H^Z, and H^O, participate in a hydroxylation of a B-ring of a flavonoid biosynthesis precursor participating in the flavonoid biosynthesis of the pelargonidin (Pgn), the cyanidin (Cyn), and the delphinidin (Dpn).for crossing flowering plants based on their pigment genotypes, comprising creating new flower color utilizing new genotype H^XH^X Pg/pg Cy/cy Dp/dp, which is heredity of pelargonidin (Pgn), cyanidin (Cyn), and delphinidin (Dpn), which are main flower pigments concerning the flower color expression.

2. (Currently Amended) A method, comprising:

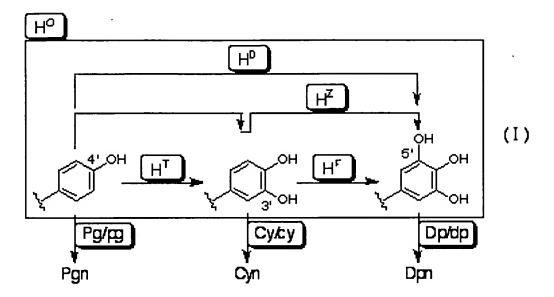
introducing a genotype D/d·E/e·H^XH^X·Pg/pg·Cy/cy·Dp/dp in a flavonoid biosynthesis for crossing flowering plants to create a new flower color,

wherein the genotype D/d·E/e·H^XH^X·Pg/pg·Cy/cy·Dp/dp is an inheritance of flower pigments, pelargonidin (Pgn), cyanidin (Cyn), and delphinidin (Dpn), for a flower color expression, and an inheritance of a double flower type or a marginal variegation type, and

wherein five multiple alleles, H^T, H^F, H^D, H^Z, and H^O, participate in a hydroxylation of a B-ring of a flavonoid biosynthesis precursor participating in the flavonoid biosynthesis of the pelargonidin (Pgn), the cyanidin (Cyn), and the delphinidin (Dpn).

flower color utilizing genotype D/d·E/e·H^XH^X·Pg/pg·Cy/cy·Dp/dp, which is heredity of pelargonidin (Pgn), cyanidin (Cyn), and delphinidin (Dpn), which are main-flower pigments concerning the flower color expression and which is heredity of double flower type, or marginal variegation type.

3. (Currently Amended) The method of claim 1, further comprising: —for crossing flowering plants based on their pigment genotypes according to claim 1, wherein precipitating the flower pigment—genotype precipitates—in and inherits—the flavonoid biosynthesis, wherein the precipitating comprises and has a route formula (I):



(wherein H^T, H^F, H^D, H^Z, and H^O are multiple alleles participating in hydroxylation of B-ring of flavonoid biosyntesis precursor participating in biosynthesis of pelargonidin (Pgn), cyanidin (Cyn), and delphinidin (Dpn). These

wherein the five multiple alleles, H^T, H^F, H^D, H^Z, and H^O, are configured to control hydroxylation at 3'-position, hydroxylation at 5'-position, hydroxylation of 3',5'-positions, hydroxylation at 3'- and 5'-positions, and hydroxylation of 5'-, and 3',5'-position, respectively.;

the expression of these five multiple alleles may be other expression method, for example, T, F, D, Z, O; the expression Pg/pg, Cy/cy and Dp/dp means the existence of gene loci corresponding to the expression of dihydroflavonol reductase (DFR) or anthocyanidin synthase (AS) participating in biosynthesis of Pgn, Cyn, and Dpn; D/d is a corolla character of double flower type, and E/e is a corolla character of marginal variegation).

- 4. (Currently Amended) The method of claim 1, for crossing flowering plants based on their pigment genotypes according to claim 1, wherein the new flower color of the flowering plants is inherited in the course of the flavonoid biosynthesis.
- 5. (Currently Amended) The method of claim 2, for crossing flowering plants based on their pigment genotypes according to claim 2, wherein the new flower color of the flowering plants is inherited in the course of the flavonoid biosynthesis.
- 6. (Currently Amended) The method of claim 3, for crossing flowering plants based on their pigment genotypes according to claim 3, wherein the new flower color of the flowering plants is inherited in the course of the flavonoid biosynthesis.
- 7. (Currently Amended) The method of claim 1, for crossing flowering plants based on their pigment genotypes according to any one of claim 1 or 2, wherein said the new flower color is maternally inherited.
- 8. (Withdrawn) A quick reference cap guide which determine the combination of crossing plants based on flower pigment genotype for creating a flower color, which displays the combination of multiple allele according to any one of claim 1 or 2 taking gametes of pollen parents as a row and gametes of seed parent as a line.

- 9. (Withdrawn) A quick reference cap guide which determine the flower color from the combination of crossing plants based on flower pigment genotype, which displays the combination of multiple allele according to any one of claims 1 or 2 taking gametes of pollen parents as a row and gametes of seed parent as a line to understand the flower color.
- 10. (Withdrawn) Use of the quick reference cap guide of multiple allele according to claim 8 for crossing based on a flower pigment genotype for creating new flower color.
- 11. (Withdrawn) Use of the quick reference cap guide of multiple allele according to claim 9 for crossing based on a flower pigment genotype for creating new flower color.
- 12. (New) The method of claim 2, wherein the new flower color is maternally inherited.
- 13. (New) The method of claim 3, wherein a flower color expression of these five multiple alleles may produced by another expression, T, F, D, Z, O,

wherein the expression Pg/pg, Cy/cy and Dp/dp are the existence of gene loci corresponding to the expression of dihydroflavonol reductase (DFR) or anthocyanidin

synthase (AS) participating in the flavonoid biosynthesis of the pelargonidin (Pgn), the cyanidin (Cyn), and the delphinidin (Dpn),

wherein D/d is a corolla character of a double flower type, and wherein E/e is a corolla character of a marginal variegation.

14. (New) The method of claim 1, further comprising:

before the introducing, establishing or analyzing the genotype $H^XH^X\cdot Pg/pg\cdot Cy/cy\cdot Dp/dp$ in the flavonoid biosynthesis in flowering plants to be crossed; and

selecting two flowering plants to be crossed based on the established or analyzed genotype.